

	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile	
	545	550 555 560
5	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn	
	565	570 575
	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln	
	580	585 590
10	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp	
	595	600 605
	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp	
	610	615 620
15	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn	
	625	630 635 640
20	Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val	
	645	650 655
	Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys	
	660	665 670
25	Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu	
	675	680 685
	Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro	
	690	695 700
30	Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp	
	705	710 715 720
	Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu	
	725	730 735
35	Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys	
	740	745 750
40	Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp	
	755	760 765
	Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn	
	770	775 780
45	Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile	
	785	790 795 800
	Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn	
	805	810 815
50	Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His	
	820	825 830

	Ser	His	His	Phe	Thr	Leu	Asp	Ile	Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn
			835					840					845			
5	Glu	Asp	Leu	Gly	Val	Trp	Val	Ile	Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly
		850					855					860				
	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	Phe	Leu	Glu	Glu	Lys	Pro	Leu	Leu
	865					870					875				880	
10	Gly	Glu	Ala	Leu	Ala	Arg	Val	Lys	Arg	Ala	Glu	Lys	Lys	Trp	Arg	Asp
				885						890					895	
	Lys	Arg	Glu	Lys	Leu	Gln	Leu	Glu	Thr	Asn	Ile	Val	Tyr	Lys	Glu	Ala
15				900					905					910		
	Lys	Glu	Ser	Val	Asp	Ala	Leu	Phe	Val	Asn	Ser	Gln	Tyr	Asp	Arg	Leu
		915						920					925			
20	Gln	Val	Asp	Thr	Asn	Ile	Ala	Met	Ile	His	Ala	Ala	Asp	Lys	Arg	Val
	930						935						940			
	His	Arg	Ile	Arg	Glu	Ala	Tyr	Leu	Pro	Glu	Leu	Ser	Val	Ile	Pro	Gly
	945					950					955				960	
25	Val	Asn	Ala	Ala	Ile	Phe	Glu	Glu	Leu	Glu	Gly	Arg	Ile	Phe	Thr	Ala
					965					970					975	
	Tyr	Ser	Leu	Tyr	Asp	Ala	Arg	Asn	Val	Ile	Lys	Asn	Gly	Asp	Phe	Asn
30				980					985					990		
	Asn	Gly	Leu	Leu	Cys	Trp	Asn	Val	Lys	Gly	His	Val	Asp	Val	Glu	Glu
		995						1000					1005			
35	Gln	Asn	Asn	His	Arg	Ser	Val	Leu	Val	Ile	Pro	Glu	Trp	Glu	Ala	Glu
	1010						1015					1020				
	Val	Ser	Gln	Glu	Val	Arg	Val	Cys	Pro	Gly	Arg	Gly	Tyr	Ile	Leu	Arg
	1025					1030					1035				1040	
40	Val	Thr	Ala	Tyr	Lys	Glu	Gly	Tyr	Gly	Glu	Gly	Cys	Val	Thr	Ile	His
					1045					1050					1055	
	Glu	Ile	Glu	Asp	Asn	Thr	Asp	Glu	Leu	Lys	Phe	Ser	Asn	Cys	Val	Glu
45				1060					1065					1070		
	Glu	Glu	Val	Tyr	Pro	Asn	Asn	Thr	Val	Thr	Cys	Asn	Asn	Tyr	Thr	Gly
		1075						1080					1085			
50	Thr	Gln	Glu	Glu	Tyr	Glu	Gly	Thr	Tyr	Thr	Ser	Arg	Asn	Gln	Gly	Tyr
	1090						1095						1100			
	Asp	Glu	Ala	Tyr	Gly	Asn	Asn	Pro	Ser	Val	Pro	Ala	Asp	Tyr	Ala	Ser
	1105					1110					1115				1120	

Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys  
1125 1130 1135

5 Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr  
1140 1145 1150

Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile  
1155 1160 1165

10 Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu  
1170 1175 1180

Leu Leu Met Glu Glu  
1185

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3567

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT	48
Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser	
1 5 10 15	

35

AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT	96
Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn	
20 25 30	

40

TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC	144
Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn	
35 40 45	

45

TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG	192
Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp	
50 55 60	

50

GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA	240
Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu	
65 70 75 80	

CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT	288
Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile	
85 90 95	